

IN THE CLAIMS

The status of each claim is listed below.

1. (Currently Amended) A transformed microorganism belonging to enterobacteria and having L-glutamic acid productivity, into which a citrate synthase gene obtained ~~derived~~ from a coryneform bacterium is introduced.

2. (Original) The microorganism of claim 1 wherein the coryneform bacterium is *Brevibacterium lactofermentum*.

Claims 3-5: Canceled.

6. (Previously Presented) The microorganism of claim 1 wherein the microorganism belonging to enterobacteria is a bacterium belonging to the genus *Enterobacter* or *Klebsiella*.

7. (Previously Presented) The microorganism of claim 2 wherein the microorganism belonging to enterobacteria is a bacterium belonging to the genus *Enterobacter* or *Klebsiella*.

8. (Previously Presented) The microorganism of claim 6 wherein the bacterium is *Enterobacter agglomerans* or *Klebsiella planticola*.

9. (Previously Presented) The microorganism of claim 7 wherein the bacterium is *Enterobacter agglomerans* or *Klebsiella planticola*.

10. (Previously Presented) A process for producing L-glutamic acid comprising the steps of culturing the microorganism of claim 1 in a liquid medium to produce and accumulate L-glutamic acid in the medium and collecting the L-glutamic acid from the medium.

11. (Previously Presented) A process for producing L-glutamic acid comprising isolating a coryneform bacterium citrate synthase gene by amplifying the gene with oligonucleotide primers comprising SEQ ID NOS: 1 and 2;
transforming an enterobacteria with said isolated citrate synthase gene;
culturing said enterobacteria in a liquid medium to produce and accumulate the L-glutamic acid; and
collecting the L-glutamic acid produced.

12. (Previously Presented) The process of Claim 11, wherein the coryneform bacteria is *Brevibacterium lactofermentum*.

13. (Previously Presented) The process of Claim 11, wherein the enterobacteria is of the genus *Enterobacter* or *Klebsiella*.

14. (Previously Presented) The process of Claim 11, wherein the enterobacteria is *Enterobacter agglomerans* or *Klebsiella planticola*.

15. (Previously Presented) The process of claim 11, wherein the oligonucleotide primers comprise SEQ ID NO:1 and SEQ ID NO:2.

16. (Currently Amended) ~~The An-enterobacteria~~ microorganism of claim 1, ~~having L-glutamic acid productivity, which has introduced a DNA encoding a coryneform bacterium citrate synthase, wherein the citrate synthase gene is obtained from DNA is obtainable from~~ corynebacterium chromosomal DNA by the polymerase chain reaction using oligonucleotide primers based on the nucleotide sequence of Corynebacterium glutamicum citrate synthase gene.

17. (Currently Amended) The microorganism of claim 16 ~~15~~, wherein the oligonucleotide primers comprise SEQ ID NO:1 and SEQ ID NO:2.

18. (Previously Presented) A process for producing L-glutamic acid comprising the steps of culturing the microorganism of claim 16 in a liquid medium to produce and accumulate L-glutamic acid in the medium and collecting the L-glutamic acid from the medium.

19. (Previously Presented) A process for producing L-glutamic acid comprising culturing the microorganism of claim 17 in a liquid medium to produce and accumulate L-glutamic acid in the medium and collecting the L-glutamic acid from the medium.

20. (New) The microorganism of Claim 1, wherein the microorganism belonging to enterbacteria belongs to the genus *Serratia*.

21. (New) The microorganism of Claim 1, wherein the microorganism belonging to enterbacteria belongs to the genus *Erwinia*.

22. (New) The microorganism of Claim 1, wherein the microorganism belonging to enterbacteria belongs to the genus *Escherichia*.

23. (New) The microorganism of Claim 1, wherein the coryneform bacterium belongs to a genus selected from the group consisting of *Corynebacterium* and *Brevibacterium*.

24. (New) The process of Claim 11, wherein the microorganism belonging to enterbacteria belongs to the genus *Serratia*.

25. (New) The process of Claim 11, wherein the microorganism belonging to enterbacteria belongs to the genus *Erwinia*.

26. (New) The process of Claim 11, wherein the microorganism belonging to enterbacteria belongs to the genus *Escherichia*.

27. (New) The process of Claim 11, wherein the coryneform bacterium belongs to a genus selected from the group consisting of *Corynebacterium* and *Brevibacterium*.

SUPPORT FOR THE AMENDMENTS

Claim 1 has been amended to recite a “transformed microorganism” and that the citrate synthase gene is “obtained from a coryneform bacterium,” both of which are supported by the specification as originally filed. Claim 16 has been amended to depend from Claim 1. Claim 17 has been amended to depend from Claim 16. Newly-added Claims 20-27 are supported by the specification at pages 12-18.

No new matter is believed to have been introduced by the amendments submitted above.